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(1) GENERAL INFORMATION:

(1) APPLICANT: Simons, Michael
Volk, Rudiger
Horowitz, Arie

(ii) TITLE OF INVENTION: Stimulation of angiogenesis
via enhanced endothelial expression of syndecan-4
core proteins

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: David Prashker, Esq.
(B) STREET: P.O. Box 5387
(C) CITY: Magnolia
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 01930

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 3.50 inch, 1.40 Mb storage
(B) COMPUTER: Dell PC
(C) OPERATING SYSTEM: MS DOS
(D) SOFTWARE: Microsoft Word version 97

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/145,916
(B) FILING DATE: September 2, 1998
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: David Prashker, Esq.
(B) REGISTRATION NUMBER: 29,693
(C) REFERENCE/DOCKET NUMBER: BIS-039

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (978) 525-3794

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 762 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGACGTG CGGCCTCTG GCTTGGCTC TGCCTCGCTGG CGCTGCCCT GCAGCCTGCC 60
CTCCCGAAA TTGTCACCGC AAATGTGCCT CCTGAAGACC AAGATGGCTC TGGGGACGAC 120
TCAGACAAC TCTCTGGCTC AGGCACAGGT GCTTTGCCAG ATATGACTTT GTCACGGCAG 180
ACACCTTCCA CTTGGAAGGA TGTGTGGCTC CTGACAGCTA CACCCACAGC TCCAGAACCC 240
ACCAAGCAGGG ATACCGAGGC CACCCCTCACC TCTATCCTGC CGGCTGGAGA GAAGCCTGAG 300
GAGGGAGAGC CCGTGGCCCA CGTGGAAAGCA GAGCCTGACT TCACTGCTCG GGACAAGGAG 360
AAGGAGGCCA CCACCAGGCC TAGGGAGACC ACACAGCTCC CAGTCACCCA ACAGGCCCTCA 420
ACAGCAGCCA GAGCCACAC GGGCCAGGCA TCTGTCACGT CTCATCCCCA CGGGGATGTG 480
CAACCTGGCC TCCACGAGAC CTTGGCTCCC ACAGCACCCG GCCAACCTGA CCATCAGCCT 540
CCAAGTGTGG AGGATGGAGG CACTTCTGTC ATCAAAGAGG TTGTGGAGGA TGAAACTACC 600
AATCAGCTTC CTGCAGGAGA GGGCTCTGGA GAACAAAGACT TCACCTTGA AACATCTGGG 660
GAGAACACAG CTGTGGCTGG CGTCGAGCCT GACCTTCGGA ATCAGTCCCC AGTGGATGAA 720
GGAGCCACAG GTGCTTCTCA GGGCCTTTG GACAGGAAGG AA 762

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCAGGAGGG AGGGAGCCAG AGGAAAAGAA GAGGAGGAGA AGGAGGAGGA CCCGGGGAGG 60
GAGGCCGCAG GCAGGGAGGAG GAGGGGCGCA GCCGCGGAGC CAGTGGCCCC GCTTGGACGC 120
GCTGCTCTCC AGATACCCCC GGAGCTCCAG CGCGCGGGAT CGCGCGCTCC CGCCGCTCTG 180
CCCCTAAACT TCTGCCGTAG CTCCCTTTCA AGCCAGCGAA TTTATTCCCTT AAAACCAGAA 240
ACTGAACCTC GGCACGGGAA AGGAGTCCGC GGAGGAGCAA AACCACAGCA GAGCAAGAAG 300
AGCTTCAGAG AGCAGCCTTC CGGGAGCACC AACTCCGTGT CGGGAGTGCA GAAACCAACA 360
AGTGAGAGGG CGCCGCGTTC CGGGGGCGCA GCTGCGGGCG GCGGGAGCAG GCGCAGGAGG 420
AGGAAGCGAG CGCCCCCGAG CCCCAGGCC GAGTCCCCGA GCCTGAGCCG CAATCGCTGC 480
GGTACTCTGC TCCGGATTG TGTCGCGCGG CTCGCCGAGC GCTGGGCAGG AGGCTTCGTT 540
TTGCCCTGGT TGCAAGCAGC GGCTGGGAGC AGCCGGTCCC TGGGAAATAT GCGGCGCGCG 600
TGGATCCTGC TCACCTTGGG CTTGGTGGCC TGCCTGTCGG CGGAGTCGAG AGCAGAGCTG 660
ACATCTGATA AAGACATGTA CCTTGACAAC AGCTCCATTG AAGAAGCTTC AGGAGTGTAT 720
CCTATTGATG ACGATGACTA CGCTTCTGCG TCTGGCTCGG GAGCTGATGA GGATGTAGAG 780
AGTCCAGAGC TGACAACAAAC TCGACCACCT CCAAAGATAAC TGTTGACTAG TGCTGCTCCA 840
AAAGTGGAAA CCACGACGCT GAATATACAG AACAAAGATAAC CTGCTCAGAC AAAGTCACCT 900
GAAGAAACTG ATAAAGAGAA AGTTCACCTC TCTGACTCAG AAAGGAAAAT GGACCCAGCC 960
GAAGAGGATA CAAATGTGTA TACTGAGAAA CACTCAGACA GTCTGTTAA ACGGACAGAA 1020

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Arg Arg Glu Gly Ala Arg Gly Lys Glu Glu Glu Lys Glu Glu
1 5 10 15
Asp Pro Gly Arg Glu Ala Arg Arg Gly Arg Arg Arg Gly Ala Ala Ala
20 25 30
Glu Pro Val Ala Pro Leu Gly Arg Ala Ala Leu Gln Ile Pro Pro Glu
35 40 45
Leu Gln Pro Arg Gly Ser Arg Ala Pro Ala Ala Leu Pro Leu Asn Phe
50 55 60
Cys Arg Ser Ser Leu Ser Ser Gln Arg Ile Tyr Ser Leu Lys Pro Glu
65 70 75 80
Thr Glu Pro Arg His Gly Lys Gly Val Arg Gly Gly Ala Lys Pro Gln
85 90 95
Gln Ser Lys Lys Ser Phe Arg Glu Gln Pro Ser Arg Ser Thr Asn Ser
100 105 110
Val Ser Gly Val Gln Lys Pro Thr Ser Glu Arg Ala Pro Arg Ser Arg
115 120 125
Gly Ala Ala Ala Gly Gly Ser Arg Arg Arg Arg Arg Lys Arg Ala
130 135 140
Pro Pro Ser Pro Glu Pro Glu Ser Pro Ser Leu Ser Arg Asn Arg Cys
145 150 155 160
Gly Thr Leu Leu Arg Ile Arg Val Arg Gly Leu Ala Glu Arg Trp Ala
165 170 175
Gly Gly Phe Val Leu Pro Trp Leu Gln Ala Ala Gly Ser Ser Arg
180 185 190
Ser Leu Gly Asn Met Arg Arg Ala Trp Ile Leu Leu Thr Leu Gly Leu
195 200 205
Val Ala Cys Val Ser Ala Glu Ser Arg Ala Glu Leu Thr Ser Asp Lys
210 215 220

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Asp Met Tyr Leu Asp Asn Ser Ser Ile Glu Glu Ala Ser Gly Val Tyr
225 230 235 240
Pro II Asp Asp Asp Tyr Ala Ser Ala Ser Gly Ser Gly Ala Asp
245 250 255
Glu Asp Val Glu Ser Pro Glu Leu Thr Thr Arg Pro Leu Pro Lys
260 265 270
Ile Leu Leu Thr Ser Ala Ala Pro Lys Val Glu Thr Thr Leu Asn
275 280 285
Ile Gln Asn Lys Ile Pro Ala Gln Thr Lys Ser Pro Glu Glu Thr Asp
290 295 300
Lys Glu Lys Val His Leu Ser Asp Ser Glu Arg Lys Met Asp Pro Ala
305 310 315 320
Glu Glu Asp Thr Asn Val Tyr Thr Glu Lys His Ser Asp Ser Leu Phe
325 330 335
Lys Arg Thr Glu
340

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1079 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCCCCGCGC GCTGCTGAGC CGTCCTTGCG GCACGSSGAT GCCCGCGGAG CTGCGGCCGCC 60
TCGCGGTGCT GCTGCTGCTG CTCAGCGCCC GCGCAGCGCT GGCTCAGCCG TGGCGCAATG 120
AGAACTACGA GAGGCCGGTG GACCTGGAGG GCTCTGGGGA TGATGATCCC TTTGGGGACG 180
ATGAACTGGA TGACATCTAC TCGGGCTCCG GCTCAGGCTA TTTTGAGCAG GAGTCAGGGT 240
TGGAGACAGC GGTCAAGCTC ACCACGGACA CGTCCGTCCC ACTGCCACC ACGGTGGCCG 300
TGCTGCCTGT CACCTTGGTG CAGCCCATGG CAACACCCCTT TGAGCTGTT CCCACAGAGG 360
ACACGTCCCC TGAGCAAACA ACCAGCGTCT TGTATATCCC CAAGATAACA GAAGCACCAAG 420
TGATCCCCAG CTGGAAAACA ACCACCGCCA GTACCACTGC CAGTGACTCC CCCAGTACCA 480
CCTCCACCAAC CACCACACG GCTGCTACCA CCACCAAC CACCACCAAC ATCAGCACCA 540
CTGTGGCCAC CTCCAAGCCC ACCACTACCC AGAGGTTCTT GCCCCCCCTT GTCACCAAGG 600
CAGCCACCAAC CGGGGCCACC ACCCTGGAGA CGCCCAACCAC CTCCATCCCT GAAACCAGTG 660
TCCTGACAGA GGTGACCAACA TCACGGCTTG TCCCCCTCCAG CACAGCCAAG CCGAGGTCCC 720
TGCCAAAACC AAGCACTTCC AGGACTGCAG AACCCACGGA AAAAGCACT GCCTTGCTT 780
CCAGCCCCAC CACGCTGCCA CCCACAGAAG CCCCCCAGGT GGAGCCAGGG GAGTTGACGA 840
CAGTCCTCGA CAGTGACCTG GAAGTCCCAA CCAGTAGTGG CCCCCAGGGGG GACTTCGAGA 900
TCCAGGAGGA GGAGGAGACA ACTCGTCCTG AGCTGGCAA TGAGGTGGTG GCAGTGGTGA 960
CACCACCAAGC AGCACCGGGG CTGGGCAAGA ATGCAGAGCC GGGGCTCATC GACAACACAA 1020
TAGAGTCGGG CAGCTGGCT GCTCAGCTCC CCCAGAAAAA CATCCTGGAG AGGAAGGAA 1079

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCGCCTG TCTGCCTGTT TGCGCCGCTG CTGCTGTTGC TCCTCGGAGG TTTCCCCGTC 60
GCCCGAGGCG AGTCGATTGAG AGAGACTGAG GTCATAGACC CCCAGGACCT CCTGGAAGGC 120
AGATACTTCT CTGGAGCCCT CCCGGACGAT GAAGACGCTG GGGGCCTTGA GCAGGACTCT 180
GACTTGAGC TGTCGGGTTC CGGAGATCTA GATGACACGG AGGAGCCAG GACCTTCCCT 240
GAGGTGATTG CACCCTGGT GCCACTAGAT AACCACATCC CCGAGAATGC CCAGCCTGGC 300

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ATCCGTGTCC CCTCAGAGCC CAAGGAAC TG GAAGAGAATG AGGTCAATTCC CAAAAGGGTC 360
CCCTCCGACG TGGGGGATGA CGATGTGTCC AACAAAGTGT CCATGTCCAG CACTTCCCAG 420
GGCAGCAACA TTTTGAAAG AACTGAG 447

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGAGCTCC GGGCCCGAGG CTGGTGGCTG CTGTGCGCGG CCGCCGCGCT AGTCGCCTGC 60
GCCCGCGGGG ACCCCGCCAG CAAGAGCCGG AGCTGCAGCG AAGTCCGCCA GATCTACGGG 120
GCTAAGGGCT TTAGCCTGAG CGACGTGCC CAGGCAGAGA TCTCGGGAGA GCACCTGCGG 180
ATCTGCCCCC AGGGCTACAC CTGCTGCACC AGTGAGATGG AGGAGAACCT GGCCAACCAC 240
AGCCGGATGG AGCTGGAGAC CGCACTCCAC GACAGCAGCC GTGCCCTGCA GGCTACACTG 300
GCCACCCAGC TGCATGGCAT CGATGACCAC TTCCAGCGCC TGCTGAATGA CTCGGAGCGT 360
ACACTGCAGG ATGCTTTCC CGGGGCCTTT GGGGACCTGT ACACGCAGAA CACTCGGGCC 420
TTCCGGGACC TGTATGOTGA GCTGCGTCTC TACTACCGAG GGGCCAACCT ACACCTTGAG 480
GAGACACTGG CCGAGTTCTG GGCACGGCTG CTGGAGCGTC TCTTCAAGCA GCTGCACCCC 540
CAGCTCTGC TGCCCGATGA CTATCTGGAC TGCCTGGCA AGCAGGCAGA GGCAC TGCGG 600
CCGTTGGGG ATGCCCTCG AGAACTGCGC CTGAGGGCCA CCCGTGCTTT TGTGGCGGCA 660
CGATCCTTG TGCAGGGCCT GGGTGTGGCC AGTGACGTAG TCCGAAAGGT GGCCCAGGTT 720
CCTCTGGCCC CAGAATGTT TCAGGGCTGTC ATGAAGTTGG TCTACTGTGC CCATTGCGG 780
GGAGTCCCTG GTGCCCGGCC CTGTCCCGAC TATTGCCGAA ATGTGCTCAA AGGCTGCCTT 840
GCCAACCAAGG CCGACCTGGA TGCCGAGTGG AGGAACCTCC TGGACTCCAT GGTGCTCATC 900
ACTGACAAGT TCTGGGGCCC GTAGGGCTGCG GAGAATGTCA TTGGCAGTGT GCATATGTGG 960
CTGGCGGAGG CCATCAACGC CCTCCAGGAC AACAAAGGACA CACTCACAGC TAAGGTATC 1020
CAGGGCTGCG GAAACCCCAA GGTCAATCCC CATGGCTCTG GGCCTGAGGA GAAGCGTCGC 1080
CGTGGCAAAC TGGCACTGCA GGAGAAGTCC TCCACAGGTA CTCTGGAAAA GCTGGCTCT 1140
GAGGCCAAGG CCCAGCTCCG AGACATTCA GACTACTGGA TCAGCCTCCC AGGGACACTG 1200
TGTAGTGAGA AGATGGCCAT GAGTCTGCC AGCGATGACC GCTGCTGGAA TGGGATTCC 1260
AAGGGCCGGT ACCTACCTGA GGTGATGGGT GATGGGCTGG CCAACCAGAT CAACAACCT 1320
GAAGTGGAGG TGGACATCAC CAAGCCGGAT ATGACCATCC GGCAGCAGAT CATGCAGCTC 1380
AAGATCATGA CCAACCCTTT ACGTGGCGCC TACGGTGGCA ATGATGTGGA CTTCCAGGAT 1440
GCCAGTGATG ACGGCAGTGG CTCCGGCAGC GGTGGCGGAT GCCCAGATGA CGCCTGTGGC 1500
CGGAGGGTCA GCAAGAAGAG CTCCAGCTCC CGGACCCCT TGACCCATGC CCTCCCCGGC 1560
TTGTCAAGAAC AGGAGGGACA GAAGACCTCG 1590

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
1 5 10 15
Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
20 25 30
Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
35 40 45
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
50 55 60
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His

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65	70	75	80
Ser Arg Met Glu Leu Glu Thr Ala Leu His Asp Ser	Ser Arg Ala Leu		
85	90	95	
Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp	Asp His Phe Gln		
100	105	110	
Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Asp	Ala Phe Pro Gly		
115	120	125	
Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala	Phe Arg Asp Leu		
130	135	140	
Tyr Ala Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn	Leu His Leu Glu		
145	150	155	160
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu	Arg Leu Phe Lys		
165	170	175	
Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr	Leu Asp Cys Leu		
180	185	190	
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp	Ala Pro Arg Glu		
195	200	205	
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala	Arg Ser Phe Val		
210	215	220	
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys	Val Ala Gln Val		
225	230	235	240
Pro Leu Ala Pro Glu Cys Ser Arg Ala Val Met Lys	Leu Val Tyr Cys		
245	250	255	
Ala His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys	Pro Asp Tyr Cys		
260	265	270	
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala	Asp Leu Asp Ala		
275	280	285	
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile	Thr Asp Lys Phe		
290	295	300	
Trp Gly Pro Ser Gly Ala Glu Asn Val Ile Gly Ser	Val His Met Trp		
305	310	315	320
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys	Asp Thr Leu Thr		
325	330	335	
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val	Asn Pro His Gly		
340	345	350	
Ser Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala	Leu Gln Glu		
355	360	365	
Lys Ser Ser Thr Gly Thr Leu Glu Lys Leu Val Ser	Glu Ala Lys Ala		
370	375	380	
Gln Leu Arg Asp Ile Gln Asp Tyr Trp Ile Ser Leu	Pro Gly Thr Leu		
385	390	395	400
Cys Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp	Asp Arg Cys Trp		
405	410	415	
Asn Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val	Met Gly Asp Gly		
420	425	430	
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val	Asp Ile Thr Lys		
435	440	445	
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu	Lys Ile Met Thr		
450	455	460	
Asn Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val	Asp Phe Gln Asp		
465	470	475	480
Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly	Cys Pro Asp		
485	490	495	
Asp Ala Cys Gly Arg Arg Val Ser Lys Lys Ser Ser	Ser Ser Arg Thr		
500	505	510	
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln	Gly Gln Lys		
515	520	525	

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5-15-02 : 10:02 :

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Thr Ser Ala
530

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTGCTGGGAG GTGTCATTGC TGGAGGCCTG GTGGGCCTCA TCTTGCTGT GTGCCTGGTG 60
GCTTCATGC TATAAC 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

DJ
GTCCTAGCAG CTGTCATTGC TGGTGGAGTT ATTGGCTTC TCTTGCAAT TTTTCTTATC 60
CTGCTGTTGG TG 72

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Leu Ala Ala Val Ile Ala Gly Gly Val Ile Gly Phe Leu Phe Ala
1 5 10 15
Ile Phe Leu Ile Leu Leu Leu Val
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGTTGATAG CTGTGATTGT CGGCGGTGTG GTGGGAGCCC TCTTGCTGC CTTCCCTTGTC 60
ATGCTGCTCA TCTAC 75

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTCTTGGCAG CTCTGATTGT GGGCGGCAGTA GTGGGCATCC TCTTCGCCGT TTTCCCTGATC 60
CTGCTGCTGG TGTAC 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCCGCCACTC GCCCAGAGCC TCACTACTTC TTTCTGCTCT TCCTGTTCAC CTTGGTCCTT 60
GCTGCAGCCA GGCCCAGGTG GCGGTAAC TG CCC 93

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala	Thr	Arg	Pro	Glu	Pro	His	Tyr	Phe	Phe	Leu	Leu	Phe	Leu	Phe	Thr
1							5			10				15	
Leu	Val	Leu	Ala	Ala	Ala	Arg	Pro	Arg	Trp	Arg					
			20						25						

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TCGCGACACT GCTCATCCCCA GCCATCACGA CTGCTGACGC CGGCTTCTAC CTCTGCGTGG 60
CCACCAGCCC TGCAGGGCACT GCC 83

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGCATGAAGA AGAAGGATGA AGGCAGTTAC GACTTGGGCA AGAAACCCAT CTACAAAAAA 60
GCCGCCACCA ACGAGTTCTA CGCATGA 87

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCCCGCCAGC AAGAGCCGGA GCT

23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAGGCCTCT GGGCGAGTGG GGG

23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATAGAGCTCT TGGAAACCATG GCGCCTGTCT GCC

33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGAATTCCAG GTTTTATTAT CTTTTTATC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTATTGGGC GCCGTGTAC CAGGGC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCCATGAGC TCCACCACCC TGTCG

26

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Leu Gly Lys Lys Pro Ile Tyr Lys Lys

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